

S/S  
#16

FIGURE 1A

ATG	AAG	CCG	TAC	TTC	TGC	CGT	GTC	TTT	GTC	TTC	TGC	TTC	CTA	ATC	45
M	K	P	Y	F	C	R	V	F	V	F	C	F	L	I	15
				5					10						
AGA	CTT	TTA	ACA	GGA	GAA	ATC	AAT	GGC	TCG	GCC	GAT	CAT	AGG	ATG	90
R	A	L	T	G	E	I	N	G	S	A	D	H	R	M	30
				20					25						
TTT	TCA	TTT	CAC	AAT	GGA	GGT	GTA	CAG	ATT	TCT	TGT	AAA	TAC	CCT	135
F	S	F	H	N	G	G	V	Q	I	S	C	K	Y	P	45
				35					40						
GAG	ACT	GTC	CAG	CAG	TTA	AAA	ATG	CGA	TTG	TTC	AGA	GAG	AGA	GAA	180
E	T	V	Q	Q	L	K	M	R	L	F	R	E	R	E	60
				50					55						
GTC	CTC	TGC	GAA	CTC	ACC	AAG	ACC	AAG	GGA	AGC	GGA	AAT	GCG	GTG	225
V	L	C	E	L	T	K	T	K	G	S	G	N	A	V	75
				65					70						
TCC	ATC	AAG	AAT	CCA	ATG	CTC	TGT	CTA	TAT	CAT	CTG	TCA	AAC	AAC	270
S	I	K	N	P	M	L	C	L	Y	H	L	S	N	N	90
				80					85						
AGC	GTC	TCT	TTT	TTC	CTA	AAC	AAC	CCA	GAC	AGC	TCC	CAG	GGA	AGC	315
S	V	S	F	F	L	N	N	P	D	S	S	Q	G	S	105
				95					100						
TAT	TAC	TTC	TGC	AGC	CTG	TCC	ATT	TTT	GAC	CCA	CCT	CCT	TTT	CAA	360
Y	Y	F	C	S	L	S	I	F	D	P	P	P	F	Q	120
				110					115						
GAA	AGG	AAC	CTT	AGT	GGA	GGA	TAT	TTG	CAT	ATT	TAT	GAA	TCC	CAG	405
E	R	N	L	S	G	G	Y	L	H	I	Y	E	S	Q	135
				125					130						
CTC	TGC	TGC	CAG	CTG	AAG	CTC	TGG	CTA	CCC	GTA	GGG	TGT	GCA	GCT	450
L	C	C	Q	L	K	L	W	L	P	V	G	C	A	A	150
				140					145						
TTC	GTT	GTG	GTA	CTC	CTT	TTT	GGA	TGC	ATA	CTT	ATC	ATC	TGG	TTT	495
F	V	V	V	L	L	F	G	C	I	L	I	I	W	F	165
				155					160						
TCA	AAA	AAG	AAA	TAC	GGA	TCC	AGT	GTG	CAT	GAC	CCT	AAT	AGT	GAA	540
S	K	K	K	Y	G	S	S	V	H	D	P	N	S	E	180
				170					175						
TAC	ATG	TTC	ATG	GCG	GCA	GTC	AAC	ACA	AAC	AAA	AAG	TCT	AGA	CTT	585
Y	M	F	M	A	A	V	N	T	N	K	K	S	R	L	195
				185					190						
GCA	GGT	GTG	ACC	TCA											600
A	G	V	T	S											200

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FIGURE 1B

mCRP1	MKPYFCRVFV	FCFLIRLL--	-----TGEIN	GS-----ADHR	MFSFHNGGVQ	39
mCD28	MT-----	----LRLFL	ALNFFSVQVT	ENKILVKQSP	LLVVDSEVS	38
Consensus	M.....	.....RLL..	.....	.....	.....V.	
mCRP1	ISCKYPETV-	-QQLKMRLFR	--EREV-LCE	LTKTKGSGNA	VSIKNPMLCL	34
mCD28	LSCRYSYNLL	AKEFRASLYK	GVNSDVEVCV	GNGNFTYQPQ	FRSNAEFNCD	33
Consensus	.SC.Y.....	.....L..	.....V..C.	.....	.....C.	
mCRP1	YHLSNNSVSF	FLNNPDSSQG	SYFFCSLSIF	DPPPFQERNL	SGGYL-HIYE	133
mCD28	GDFDNETVTF	RLWNLHVNHT	DIYFCKIEFM	YPPPYLDNER	SNGTIIHIKE	133
Consensus	....N..V.F	.L.N.....	..YFC.....	.PPP.....	S.G...HI.E	
mCRP1	SQLC---CQL	KL-W-LPVGC	AA-FVVLLF	GCIL-IIWFS	KKKY----GS	172
mCD28	KHLCHTQSSP	KLFWALVVVA	GVLFYGLLV	TVALCVIWTN	SRNRLLQVT	138
Consensus	..LC.....	KL.W.L.V..	...F...LL.	...L..IW..	.....	
mCRP1	SVH-DPNEY	MFMAAVNTNK	KSR-LAGVTS			200
mCD28	TMNMTPRRPG	LTRKPYQPYA	PARDFAAYRP			218
Consensus	.....P.....	.....	..R..A....	...		

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FIGURE 2A

ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG	45
M Q L K C P C F V S E G T R Q	15
CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT	90
P V W K K L H V S S G F F S G	30
CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT	135
L G L F L L L L S S L C A A S	45
GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC	180
A E T E V G A M V G S N V V L	60
AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG	225
S C I D P H R R H F N L S G L	75
TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC	270
Y V Y W Q I E N P E V S V T Y	90
TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC	315
Y L P Y K S P G I N V D S S Y	105
AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC	360
K N R G H L S L D S M K Q G N	120
TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG	405
F S L Y L K N V T P Q D T Q E	135
TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG	450
F T C R V F M N T A T E L V K	150
ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT	495
I L E E V V R L R V A A N F S	165
ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA	540
T P V I S T S D S S N P G Q E	180
CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC	585
R T Y T C M S K N G Y P E P N	195
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT	630
L Y W I N T T D N S L I D T A	210
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT	675
L Q N N T V Y L N K L G L Y D	225
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT	720
V I S T L R L P W T S R G D V	240

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	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
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TTG	TGC	TGC	GTA	GAG	AAT	VTG	GCT	CTC	CAC	CAG	AAC	ATC	ACT	AGC
L	C	C	V	E	N	V	A	L	H	Q	N	I	T	S
				245					250					255
ATT	AGC	CAG	GCA	GAA	AGT	TTC	ACT	GGA	AAT	AAC	ACA	AAG	AAC	CCA
I	S	Q	A	E	S	F	T	G	N	N	T	K	N	P
				260					265					270
CAG	GAA	ACC	CAC	AAT	AAT	GAG	TTA	AAA	GTC	CTT	GTC	CCC	GTC	CTT
Q	E	T	H	N	N	E	L	K	V	L	V	P	V	L
				275					280					285
GCT	GTA	CTG	GCG	GCA	GCG	GCA	TTC	GTT	TCC	TTC	ATC	ATA	TAC	AGA
A	V	L	A	A	A	A	F	V	S	F	I	I	Y	R
				290					295					300
CGC	ACG	CGT	CCC	CAC	CGA	AGC	TAT	ACA	GGA	CCC	AAG	ACT	GTA	CAG
R	T	R	P	H	R	S	Y	T	G	P	K	T	V	Q
				305					310					315
CTT	GAA	CTT	ACA	GAC	CAC	GCC								
L	E	L	T	D	H	A								
				320		322								966



FIGURE 2B

mB7RP1	MQLKPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLS-	SLCAASAETE	49
mCD80	MA--CNC--Q	LMQDTPL---	LKFPCPRLI-	L-LFVLLIRL	SQVSSDVDEQ	41
Consensus	M...C.C...	L....P....	L.....	L.LF.LL...	S.....	
mB7RP1	VGAMVGSNVV	LSCIDPHRRH	FNLSGLYVYW	QIENPEVSVT	YYLPYKSPGI	39
mCD80	LSKSVKDKVL	LPC-RYNsph	EDESEDRIYW	QKHDKV---	--LSVIAGKL	35
Consensus	....V...V.	L.C.....H	...S....YW	Q...V...	..L.....	
mB7RP1	NVDSSYKNRG	HLSLDSMKQG	NFSLYLKNVT	PQDTQEFTCR	VFMNTATELV	149
mCD80	KVWPEYKNR-	--TL--YDNT	TYSLIILGLV	LSDRGTYSCV	VQKKERGTYE	130
Consensus	.V...YKNR.	...L.....	..SL.....	..D.....C.	V.....	
mB7RP1	KILEEVRLR	VAANFSTPVI	STSDSSNPGQ	ERTYTCMSKN	GYPEPNLYWI	199
mCD80	VKHLALVKLS	IKADFSTPNI	TESGNPSADT	KRI-TCFASG	GFPKPRFSWL	179
Consensus	.....V.L.	...A.FSTP.I	..S.....	.R..TC...	G.P.P...W.	
mB7RP1	-NTTDSLID	TALQNTVYL	NKLGLYDVIS	TLRLPWTSRG	DVLCCVENVA	248
mCD80	ENGRELPGIN	TTISQDPESE	LYTISSQLDF	NTTRNHTIKC	LIKYGDAHVS	229
Consensus	.N.....I.	T.....	.....	.....T...	.....V.	
mB7RP1	LHQNITSISQ	AESFTGNNTK	NPQETHNNEL	KVLVPVLAVL	A-AAAFVSFI	297
mCD80	EDFTWEKPPE	DPPDSKNTLV	LFGAGFGAVI	TVVVIIVVIK	CFCKHRSCFR	279
Consensus	.....	.....N...	.....	.V.V.V.....	.....F.	
mB7RP1	IYRRTR-PHR	SYT-GPKTVQ	LELTDHA			322
mCD80	RNEASRETNN	SLTFGPPEAL	AEQTVFL			306
Consensus	...R....	S.T.GP...	.E.T...			

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FIGURE 3A

ATG	CGG	CTG	GGC	AGT	CCT	GGA	CTG	CTC	TTC	CTG	CTC	TTC	AGC	AGC	45
M	R	L	G	S	P	G	L	L	F	L	L	F	S	S	
				5					10					15	
CTT	CGA	GCT	GAT	ACT	CAG	GAG	AAG	GAA	GTC	AGA	GCG	ATG	GTA	GGC	90
L	R	A	D	T	Q	E	K	E	V	R	A	M	V	G	
				20					25					30	
AGC	GAC	GTG	GAG	CTC	AGC	TGC	GCT	TGC	CCT	GAA	GGA	AGC	CGT	TTT	135
S	D	V	E	L	S	C	A	C	P	E	G	S	R	F	
				35					40					45	
GAT	TTA	AAT	GAT	GTT	TAC	GTA	TAT	TGG	CAA	ACC	AGT	GAG	TCG	AAA	180
D	L	N	D	V	Y	V	Y	W	Q	T	S	E	S	K	
				50					55					60	
ACC	GTG	GTG	ACC	TAC	CAC	ATC	CCA	CAG	AAC	AGC	TCC	TTG	GAA	AAC	225
T	V	V	T	Y	H	I	P	Q	N	S	S	L	E	N	
				65					70					75	
GTG	GAC	AGC	CGC	TAC	CGG	AAC	CGA	GCC	CTG	ATG	TCA	CCG	GCC	GGC	270
V	D	S	R	Y	R	N	R	A	L	M	S	P	A	G	
				80					85					90	
ATG	CTG	CGG	GGC	GAC	TTC	TCC	CTG	CGC	TTG	TTC	AAC	GTC	ACC	CCC	315
M	L	R	G	D	F	S	L	R	L	F	N	V	T	P	
				95					100					105	
CAG	GAC	GAG	CAG	AAG	TTT	CAC	TGC	CTG	GTG	TTG	AGC	CAA	TCC	CTG	360
Q	D	E	Q	K	F	H	C	L	V	L	S	Q	S	L	
				110					115					120	
GGA	TTC	CAG	GAG	GTT	TTG	AGC	GTT	GAG	GTT	ACA	CTG	CAT	GTG	GCA	405
G	F	Q	E	V	L	S	V	E	V	T	L	H	V	A	
				125					130					135	
GCA	AAC	TTC	AGC	GTG	CCC	GTC	GTC	AGC	GCC	CCC	CAC	AGC	CCC	TCC	450
A	N	F	S	V	P	V	V	S	A	P	H	S	P	S	
				140					145					150	
CAG	GAT	GAG	CTC	ACC	TTC	ACG	TGT	ACA	TCC	ATA	AAC	GGC	TAC	CCC	495
Q	D	E	L	T	F	T	C	T	S	I	N	G	Y	P	
				155					160					165	
AGG	CCC	AAC	GTG	TAC	TGG	ATC	AAT	AAG	ACG	GAC	AAC	AGC	CTG	CTG	540
R	P	N	V	Y	W	I	N	K	T	D	N	S	L	L	
				170					175					180	
GAC	CAG	GCT	CTG	CAG	AAT	GAC	ACC	GTC	TTC	TTG	AAC	ATG	CGG	GGC	585
D	Q	A	L	Q	N	D	T	V	F	L	N	M	R	G	
				185					190					195	
TTG	TAT	GAC	GTG	GTC	AGC	GTG	CTG	AGG	ATC	GCA	CGG	ACC	CCC	AGC	630
L	Y	D	V	V	S	V	L	R	I	A	R	T	P	S	
				200					205					210	
GTG	AAC	ATT	GGC	TGC	TGC	ATA	GAG	AAC	GTG	CTT	CTG	CAG	CAG	AAC	675
V	N	I	G	C	C	I	E	N	V	L	L	Q	Q	N	
				215					220					225	
CTG	ACT	GTC	GGC	AGC	CAG	ACA	GGA	AAT	GAC	ATC	GGA	GAG	AGA	GAC	720
L	T	V	G	S	Q	T	G	N	D	I	G	E	R	D	
				230					235					240	

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# FIGURE 3A (Con't)

AAG	ATC	ACA	GAG	AAT	CCA	GTC	AGT	ACC	GGC	GAG	AAA	AAC	GCG	GCC	765
K	I	T	E	N	P	V	S	T	G	E	K	N	A	A	
				245				:	250					255	
ACG	TGG	AGC	ATC	CTG	GCT	GTC	CTG	TGC	CTG	CTT	GTG	GTC	GTG	GCG	810
T	W	S	I	L	A	V	L	C	L	L	V	V	V	A	
				250					265					270	
GTG	GCC	ATA	GGC	TGG	GTG	TGC	AGG	GAC	CGA	TGC	CTC	CAA	CAC	AGC	855
V	A	I	G	W	V	C	R	D	R	C	L	Q	H	S	
				275					280					285	
TAT	GCA	GGT													864
Y	A	G													
				288											

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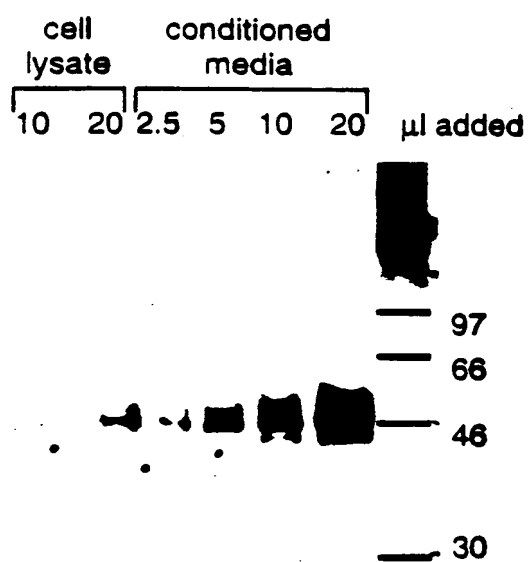


FIGURE 3B

hB7RP1	EKEVRAMVGS	DVELSCACPE	GSRFDLNDVY	VYWQTSESKT	VVTYHHPQNS	50
mB7RP1	ETEVGAMVGS	NVVLSCIDPH	RRHFNLSGLY	VYWQIENPEV	SVTYLBYKS	50
Consensus	E.EV.AMVGS	.V.LSC..P.	...F.L...Y	VYWQ.....	.VTY...P...S	
hB7RP1	SLENVDSRYR	NRALMSPAGM	LRGDFSLRLF	NVTPQDEQKF	HCLVLSQ-SL	99
mB7RP1	PGINVDSSYK	NRGHLSDSM	KQGNFSLYLK	NVTPQDTQEF	TCRVFMTAT	100
Consensus	...NVDS.Y.	NR...S...M	..G.FSL.L.	NVTPQD.Q.F	.C.V.....	
hB7RP1	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS	Q-DELTFTCT	SINGYP RPNV	143
mB7RP1	ELVKILEEVV	RLRVAANFST	PVISTSDSSN	PGQERTYTCM	SKNGYPEPNL	150
Consensus	.....L...V	.L.VAANFS.	PV.S...S...	...E.T.TC.	S.NGYP.PN.	
hB7RP1	YWINKTDNSL	LDQALQNDTV	FLNMRGLYDV	VSVLRIARTP	SVNIGCCIEEN	198
mB7RP1	YWINTTDNSL	IDTALQNNTV	YLNKLGlyDV	ISTLRLPWTS	RGDVLCCVEN	200
Consensus	YWIN.TDNSL	.D.ALQN.TV	.LN..GLYDV	.S.LR...T.	.....CC.EN	
hB7RP1	VLLQQNLTVG	SQTGNDIGER	DKITENPVST	GEKNAATWSI	LAVLCLLVVV	248
mB7RP1	VALHQNITSI	SQAESFTGNN	TKNPQETHNN	ELKVLV--PV	LAVLAAAFV	248
Consensus	V.L.QN.T..	SQ...G...	.K....K...	..K...7...	LAVL.....V	
hB7RP1	AVAIGWVCRD	RCLQHSYAG				267
mB7RP1	SFIIYR--RT	R-PHRSYTGP	KTVQLELTDH	A		276
Consensus	...I...R.	R...SY.G.	.....			



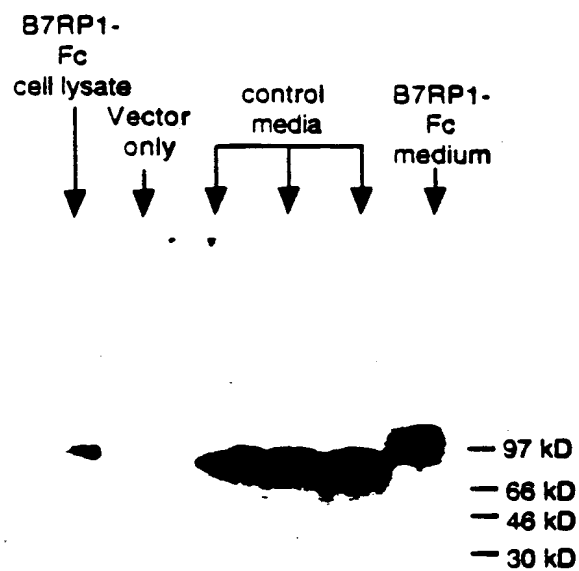
Figure 4A



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Figure 4B



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Figure 5

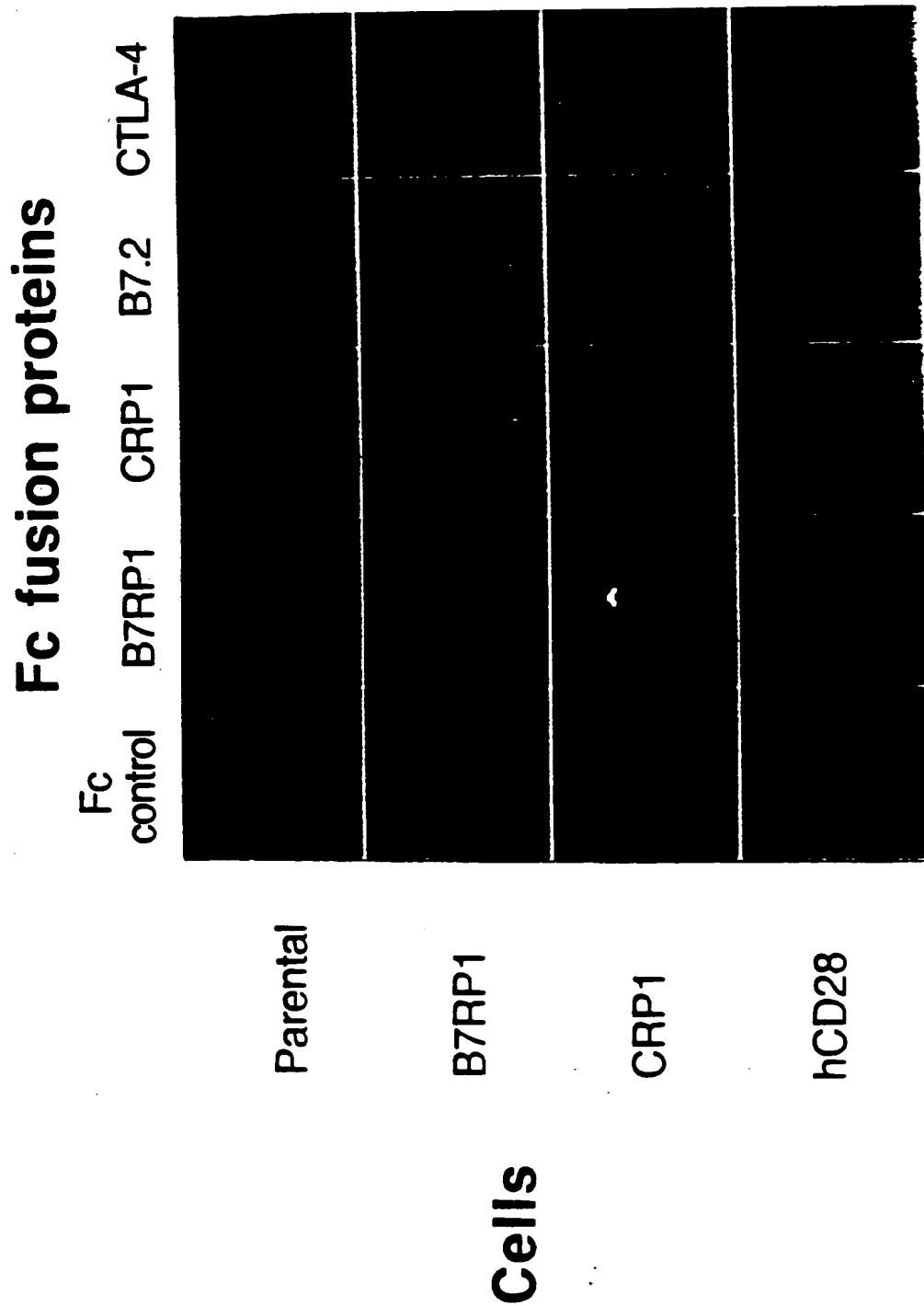




Figure 6

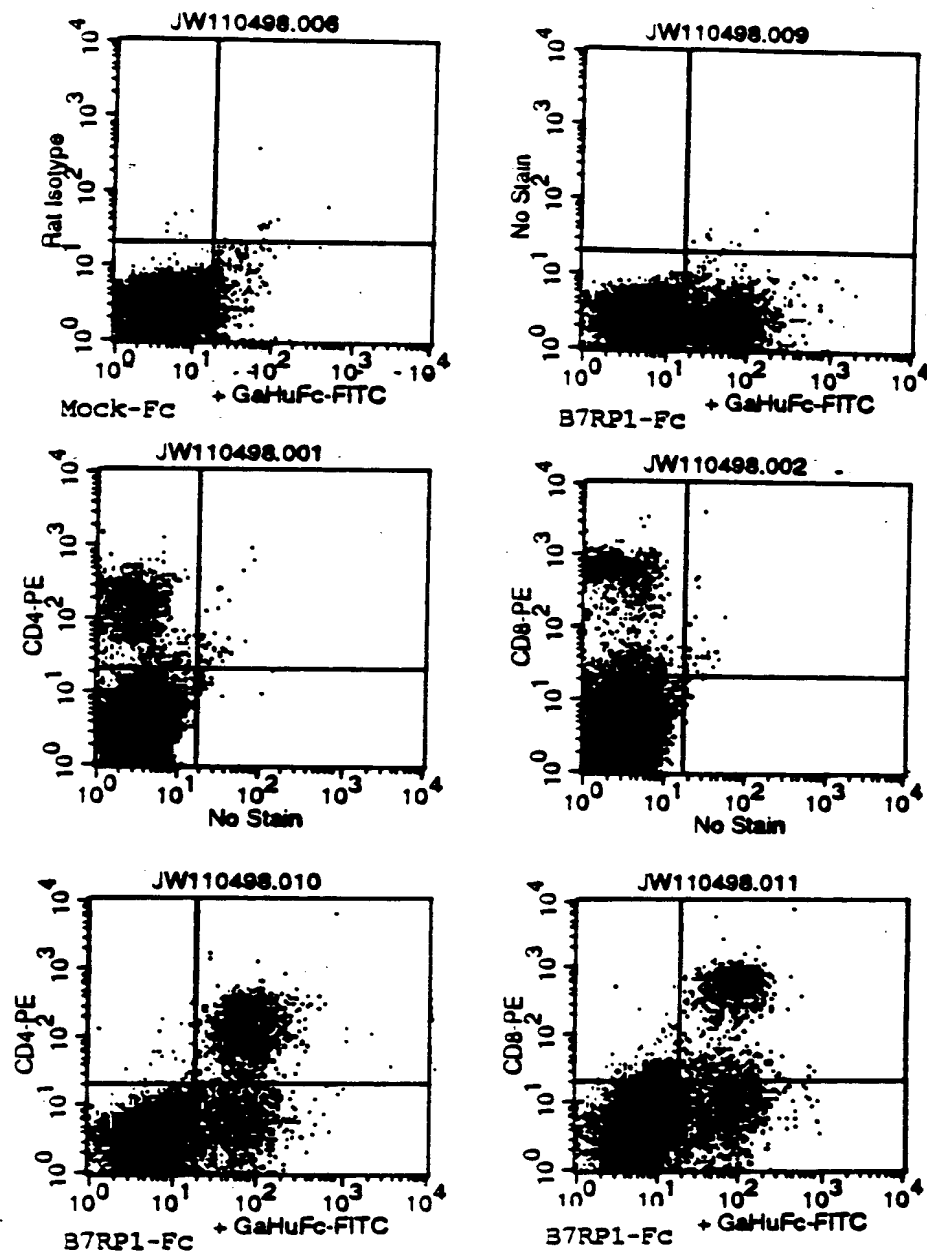
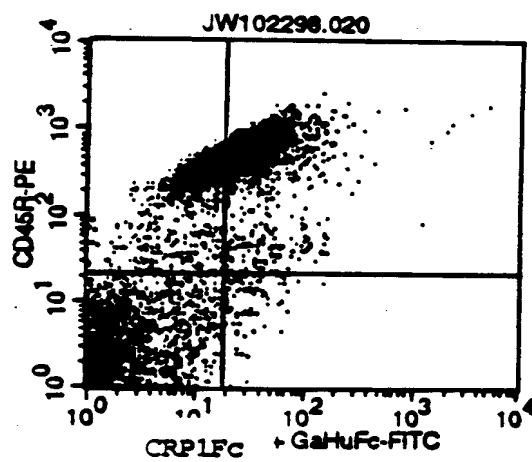
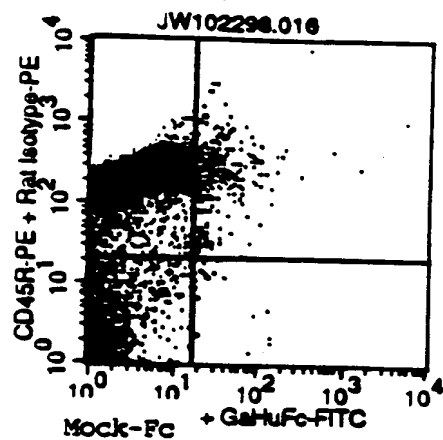
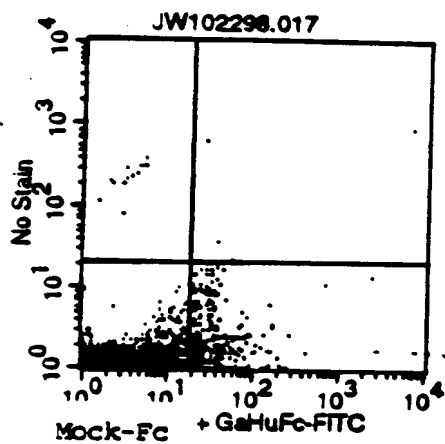




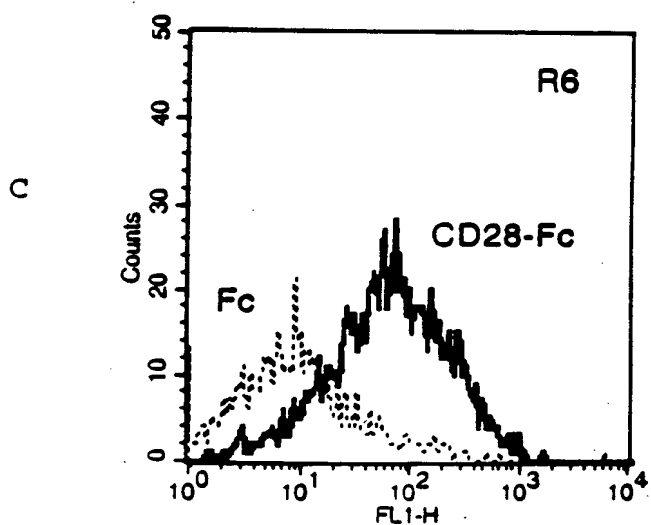
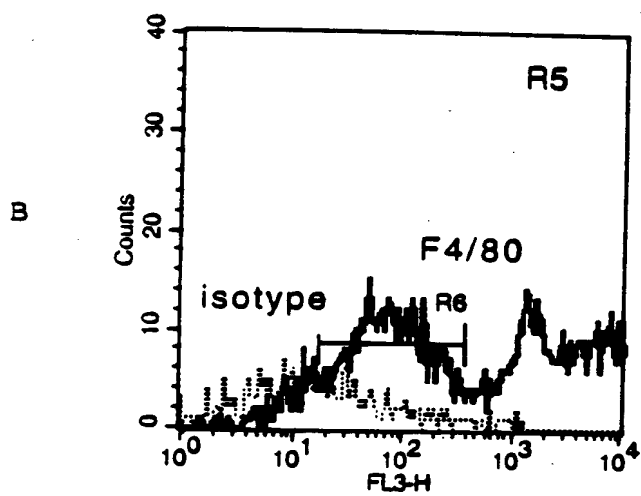
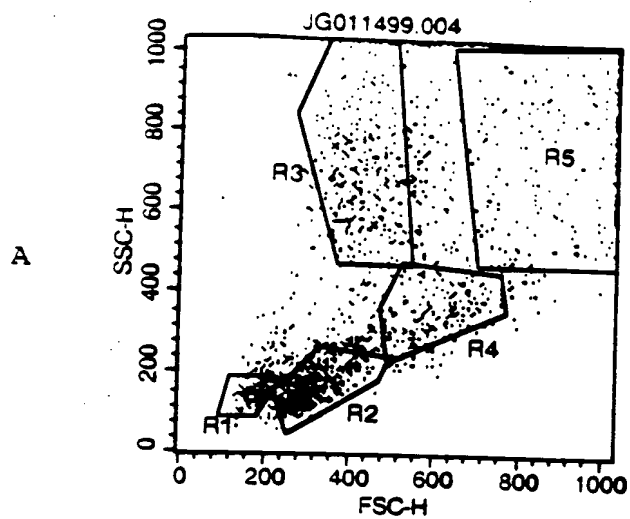
Figure 7



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Figure 3



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FIGURE 9

Con A stimulation of T-cells regulated  
by B7RP1-Fc fusion protein

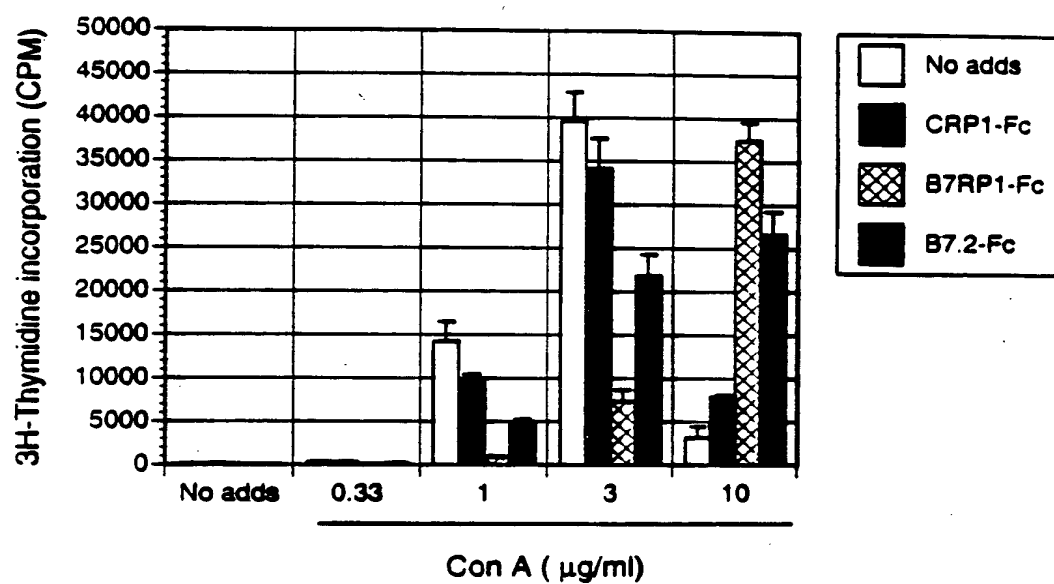




Figure 10

A Lymph node-control#10

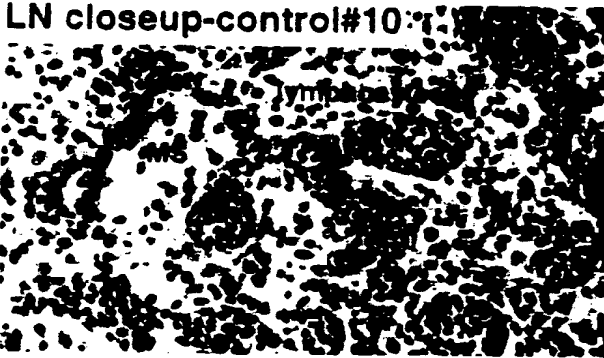


LN-WX11#40

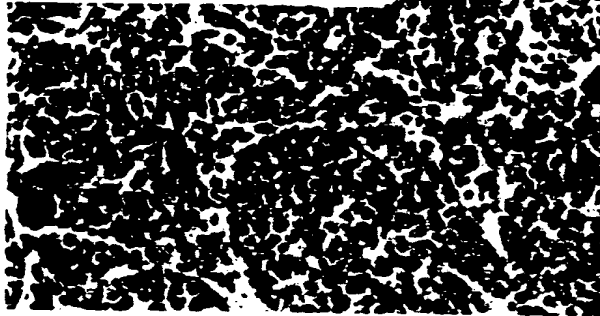


B

C LN closeup-control#10



LN closeup-WX11#40

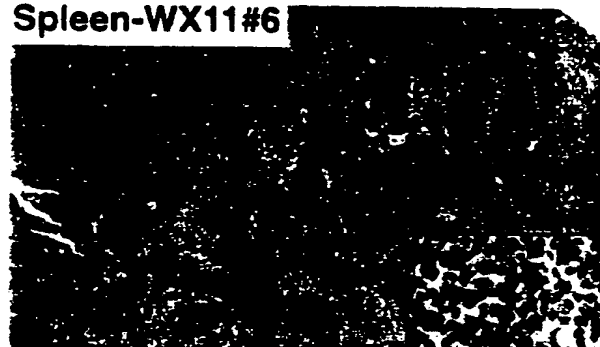


D

E Spleen-control#10



Spleen-WX11#6

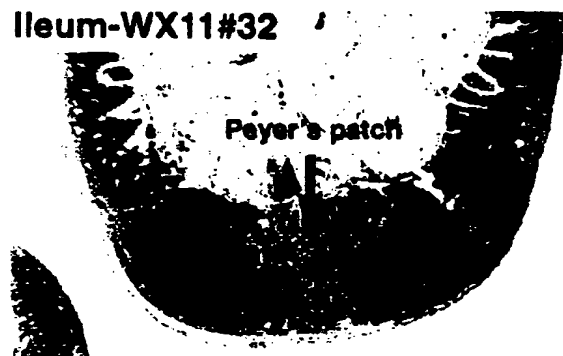


F

G Ileum-control#25



Ileum-WX11#32



H

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Figure 11

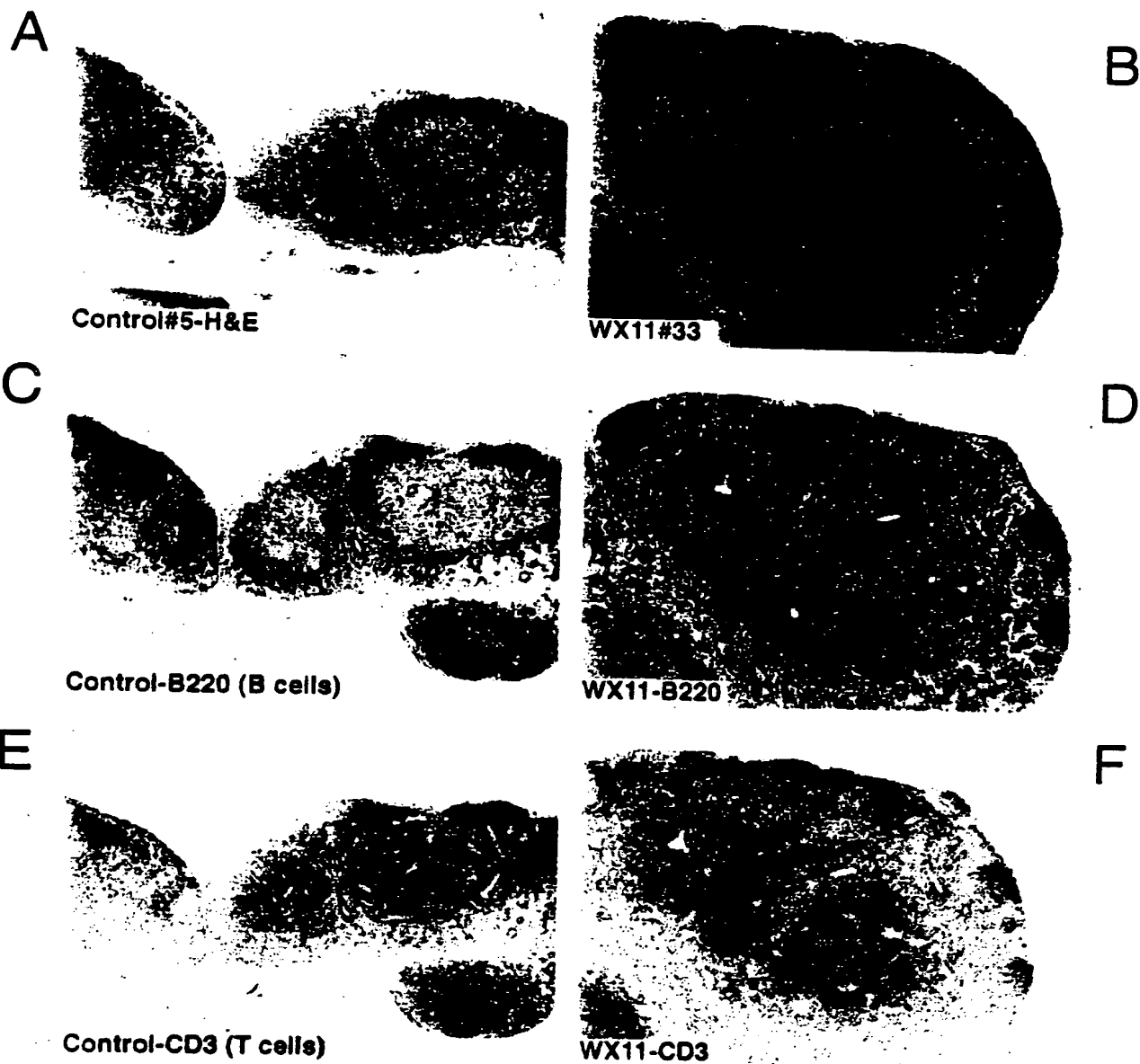




Figure 12A.

GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTTCGACCCACGCGTCCGCCCACGCG	-138
TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC	-76
CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGGCCCGAGGT	-14
CTCCGCCCCGACC	-1
ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC	45
M R L G S P G L L F L L F S S	
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC	90
L R A *D *T *Q *E K *E V R A *M V G	
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT	135
S D V E L S C A C P E G S R F	
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA	180
D L N D V Y V Y W Q T S E S K	
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC	225
T V V T Y H I P Q N S S L E N	
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC	270
V D S R Y R N R A L M S P A G	
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC	315
M L R G D F S L R L F N V T P	
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG	360
Q D E Q K F H C L V L S Q S L	
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA	405
G F Q E V L S V E V T L H V A	
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC	450
A N F S V P V V S A P H S P S	
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC	495
Q D E L T F T C T S I N G Y P	
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	
GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	

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CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	
AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC	900
Y A G A W A V S P E T E L T G	
300	
CAC GTT TGA	909
H V STOP	
302	
CCGGAGCTCACCGCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG	971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCCAGAAGGAC	1033
CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC	1095

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Figure 12B.

human	MRLGSP----	-----	-----G	L-LF-LLFSS	LRADTQEKEV	25
mouse	MQLKCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLSS	LCAASAETEV	50
Consensus	M.L..P....	.....	.....G	L.LF.LL.SS	L.A...E.EV	50
human	RAMVGSDEL	SCACPEGSRF	DLNDVYVYQ	TSESKTVVTY	HIPQNSSLEN	75
mouse	GAMVGSNVVL	SCIDPHRRHF	NLSGLYVYQ	IENPEVSVTY	YLPYKSPGIN	100
Consensus	.AMVGS.V.L	SC..P....F	.L...YVYQ	.....VTY	..P..S...N	100
human	VDSRYRNRAL	MSPAGMLRGD	FSLRLFNVTP	QDEQKFHCLV	LSQ-SLGFQE	124
mouse	VDSSYKNRGH	LSLDSMKQGN	FSLYLKNVTP	QDTQEFTCRV	FMNTATELVK	150
Consensus	VDS.Y.NR..	.S...M..G.	FSL.L.NVTP	QD.Q.F.C.V	.....	150
human	VLSVEVTLHV	AANFSVPVVS	APHSPSQ-DE	LTFTCTSING	YPRPNVYWIN	173
mouse	ILEEVVRLRV	AANFSTPVIS	TSDSSNPGQE	RTYTCMSKNG	YPEPNLYWIN	200
Consensus	.L...V.L.V	AANFS.PV.S	...S.....E	.T.TC.S.NG	YP.PN.YWIN	200
human	KTDNSLLDQA	LQNDTVFLNM	RGLYDVVSVL	RIARTPSVNI	GCCIENVLLQ	223
mouse	TTDNSLIDTA	LQNNTVYLNK	LGLYDVISTL	RLPWTSRGDV	LCCVENVALH	250
Consensus	.TDNSL.D.A	LQN.TV.LN.	.GLYDV.S.L	R...T.....	.CC.ENV.L.	250
human	QNLTVGSQTG	NDIGERDKIT	ENPVSTGEKN	AATWSILAVL	CLLVVVAVAI	273
mouse	QNITSISQAE	SFTGNNTKNP	QETHNNELKV	LV--PVLAVL	AAAAFVSFII	298
Consensus	QN.T..SQ..	...G...K..	.....K.	.....LAVL	.....V...I	300
human	GWVCRDRCLQ	HSYAGAWAVS	PETELTGHV			302
mouse	YR--RTR-PH	RSYTGPKTVQ	LE--LTDHA			322
Consensus	....R.R...	.SY.G...V.	.E..LT.H.			329

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Figure 13A

AACAAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA -111  
 CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTC -56  
 GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTTAACTGTTTCTGGCAAAC -1

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT 45  
 M K S G L W Y F F L F C L R I 15

AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 90  
 K V L T \*G \*E I N G S A N Y E M 30

TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT 135  
 F I F H N G G V Q I L C K Y P 45

GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA 180  
 D I V Q Q F K M Q L L K G G Q 60

ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG 225  
 I L C D L T K T K G S G N T V 75

TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC 270  
 S I K S L K F C H S Q L S N N 90

AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC 315  
 S V S F F L Y N L D H S H A N 105

TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA 360  
 Y Y F C N L S I F D P P P F K 120

GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT 405  
 V T L T G G Y L H I Y E S Q L 135

TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT 450  
 C C Q L K F W L P I G C A A F 150

GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA 495  
 V V V C I L G C I L I C W L T 165

AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC 540  
 K K K Y S S S V H D P N G E Y 180

ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA 585  
 M F M R A V N T A K K S R L T 195

GAT GTG ACC CTA TAA 600  
 D V T L STOP 199

TATGGAAGTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCAACTTGA 655  
 AGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTACATACA 710

00723420-112300



TCTTCTGCTGGTGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGA  
TTTTAACAGACTGCCTTGGTACTGCCGAGTCCTCTCAAAACAAACACCCCTCTTGC  
AACCAGCTTTGGAGAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTG  
TCTCCACATCTGCTCCTAGCAGTGCATCAGCCAGTAAACAAACACATTTACAAG  
AAAAATGTTTTAAAGATGCCAGGGGTACTGAATCTGCAAAGCAAATGAGCAGCCA  
AGGACCAGCATCTGTCCGCATTTCACTATCATACTACCTCTTCTTTCTGTAGGGA  
TGAGAATTCCTCTTTAATCAGTCAAGGGAGATGCTTCAAAGCTGGAGCTATTTT  
ATTTCTGAGATGTTGATGTGAAGTGTACATTAGTACATACTCAGTACTCTCCTTC  
AATTGCTGAACCCCAGTTGACCATTTTACCAAGACTTTAGATGCTTTCTTGTGCC

765  
820  
875  
930  
985  
1040  
1095  
1150  
1205

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Figure 13B

hCRP1	MKSGLWYFFLFCRLRIKVL TGEINGSANYEMFI FHNGGVQILCKYPDIVQQ	50
mCRP1	MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLT KTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD	100
mCRP1	LKMRLFREREVLCELT KTKGSGNAVSIKNPMLCLYHLSNNSVSFFLNND	100
hCRP1	HSHANYFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPVIGCAA	149
mCRP1	SSQGSYYFCSLSIFDPPPFQERNLSGGYLHIYESQLCCQLKLWLPVIGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL	199
mCRP1	FVVVLLFGCILLIWFSSKKKYSSSVHDPNSEYMFMAAVNTNKKSRLAGVTS	200

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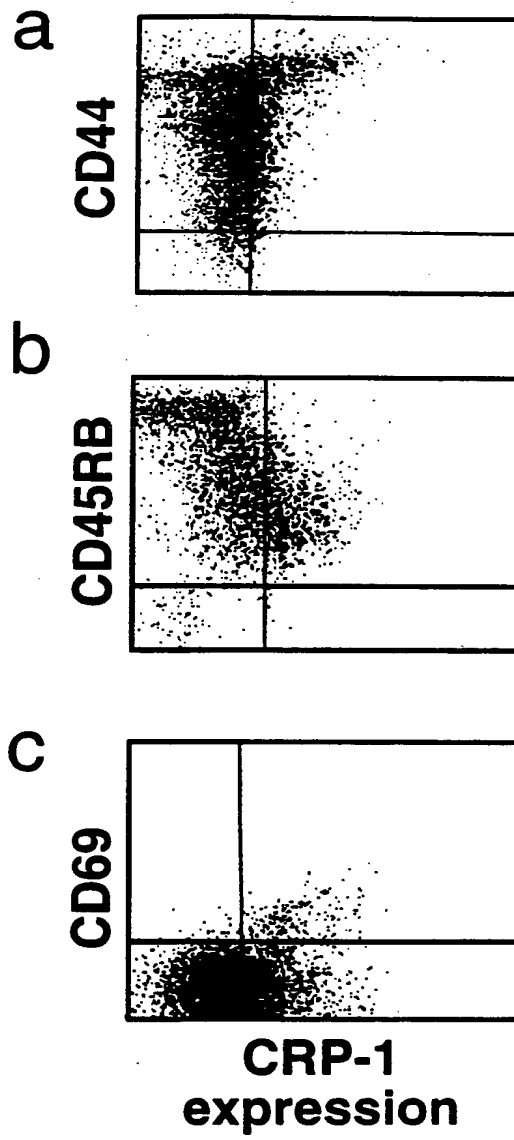
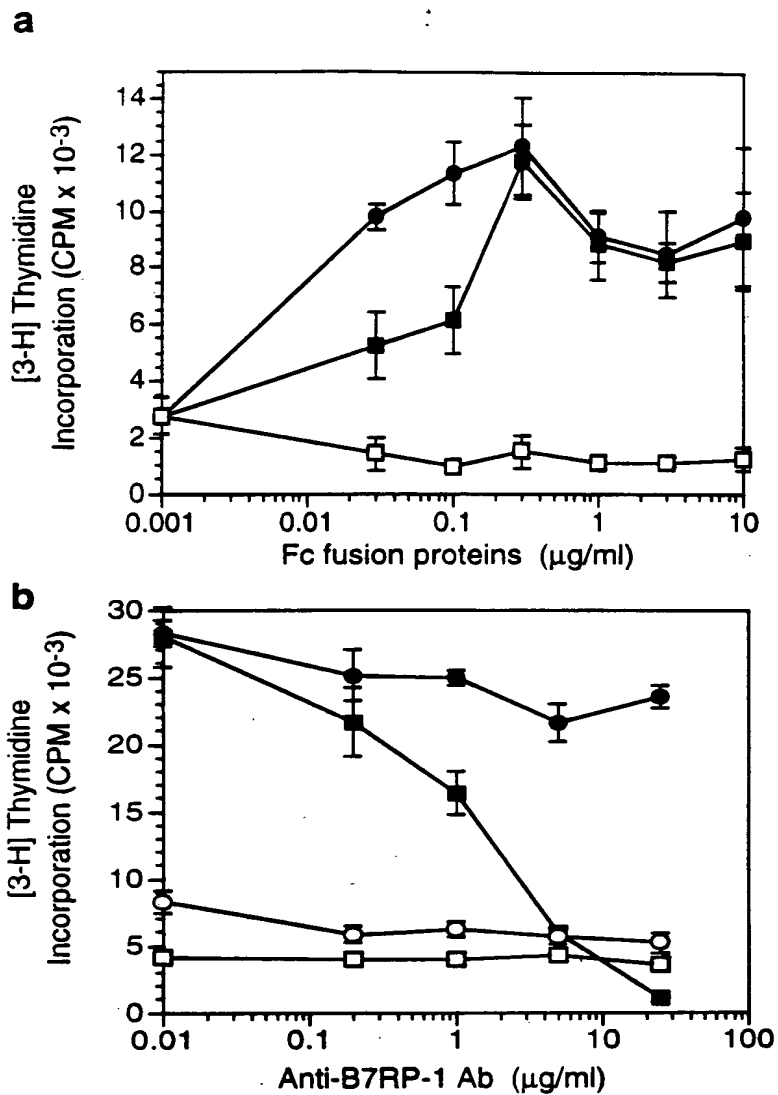


Figure 14

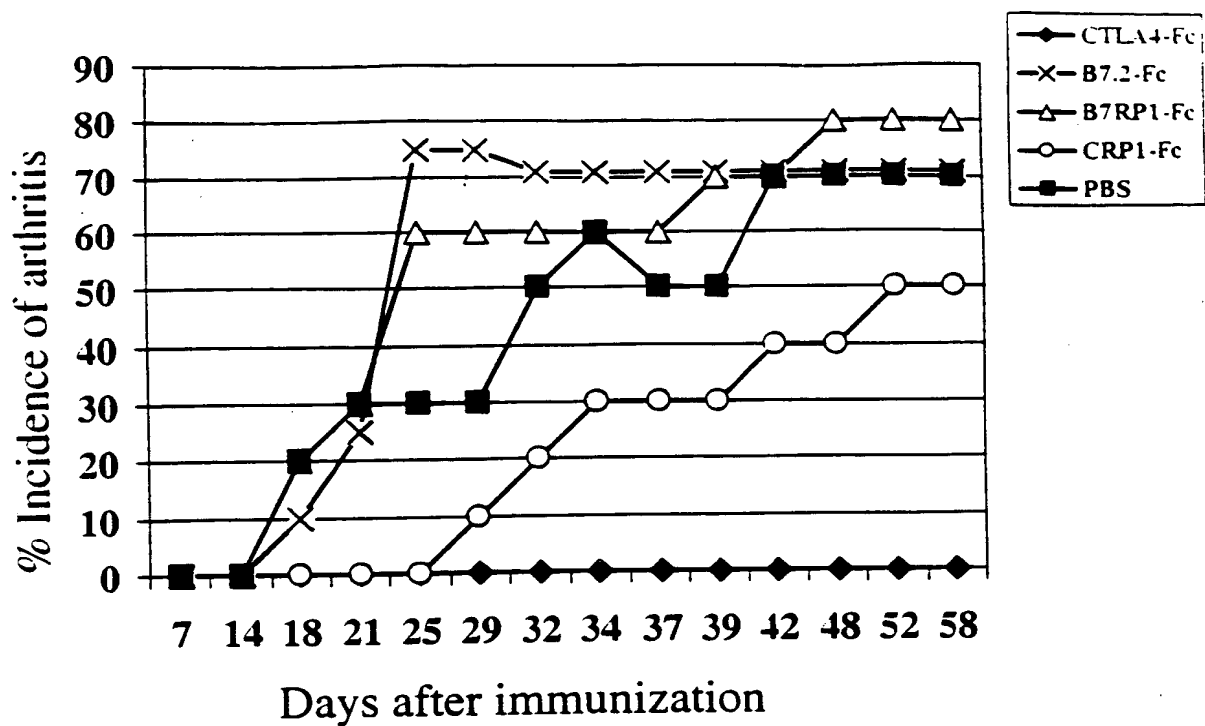




**Figure 15**



A.



B.

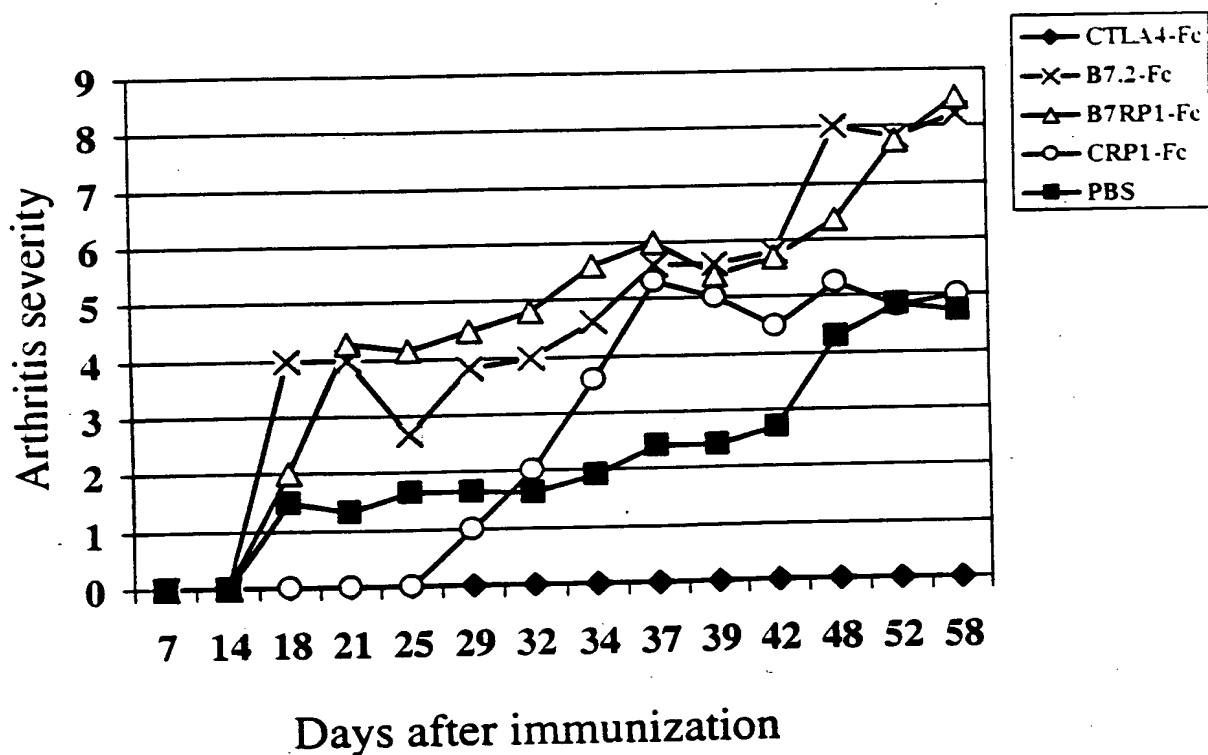
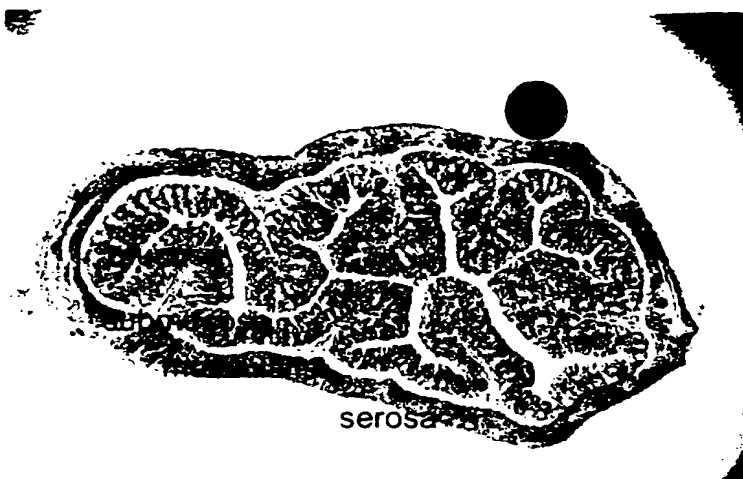


Figure 16

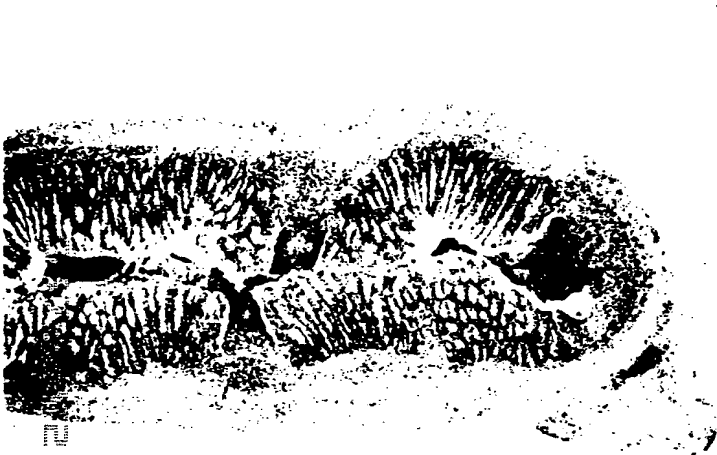




A. Control mouse#53F: Prox. colon 40X



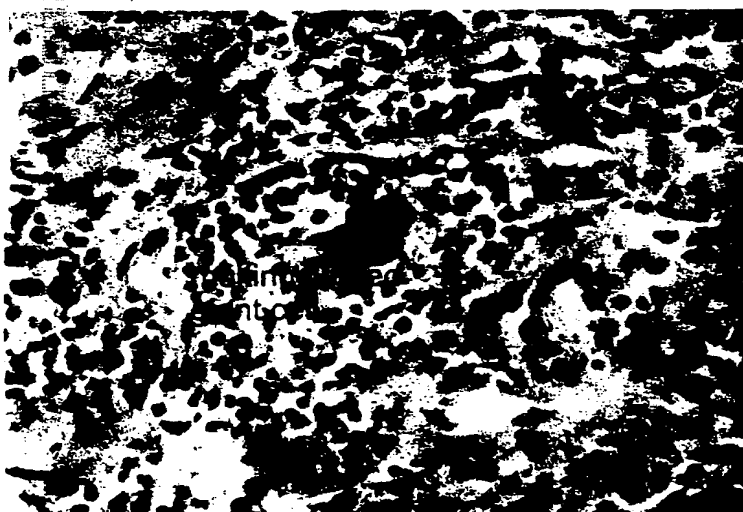
B. Mouse#111F: Prox. colon 40X



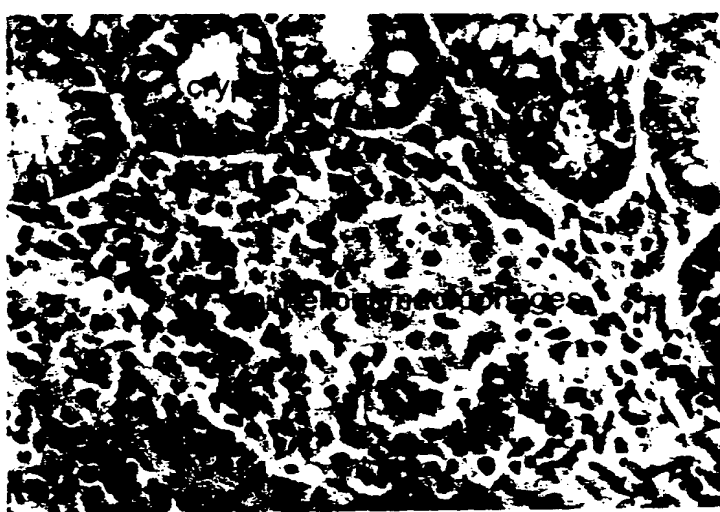
C. Mouse#111F: Prox. colon 20X



D. Mouse#111F: closeup of mucosa 100X



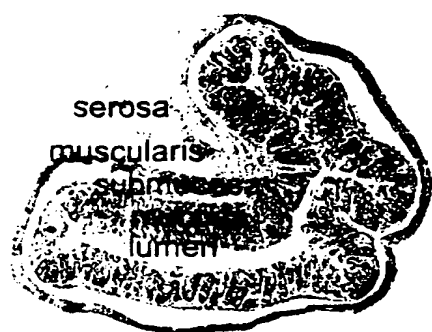
E. Mouse#112F: Giant cell, submucosa



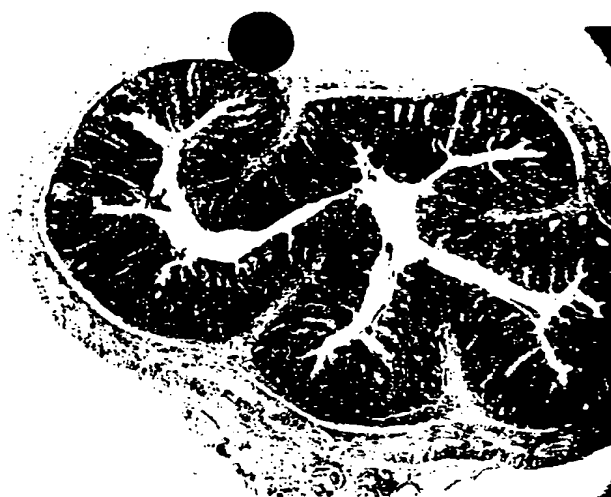
F. Mouse#112F: epithelioid macrophages

Figure 17

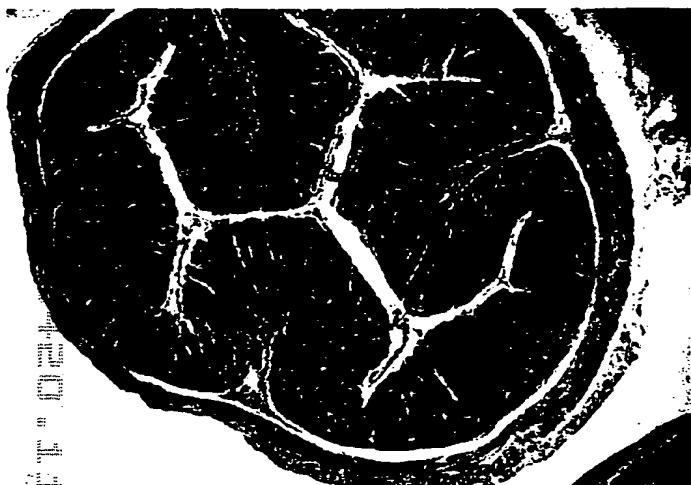




A. Control mouse#53F:Distal colon, 40X



B. mouse#111F:Distal colitis, 40X



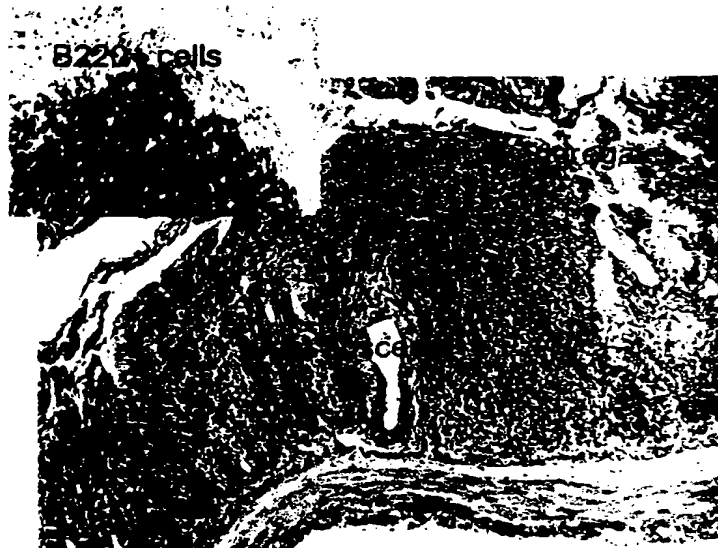
C. mouse#55M:Distal colitis, 40X



D. mouse#112F:Distal colon, 40X



E. mouse#112:CD3+ T-cells, 40X



F. mouse#112:closeup, 100X

Figure 18





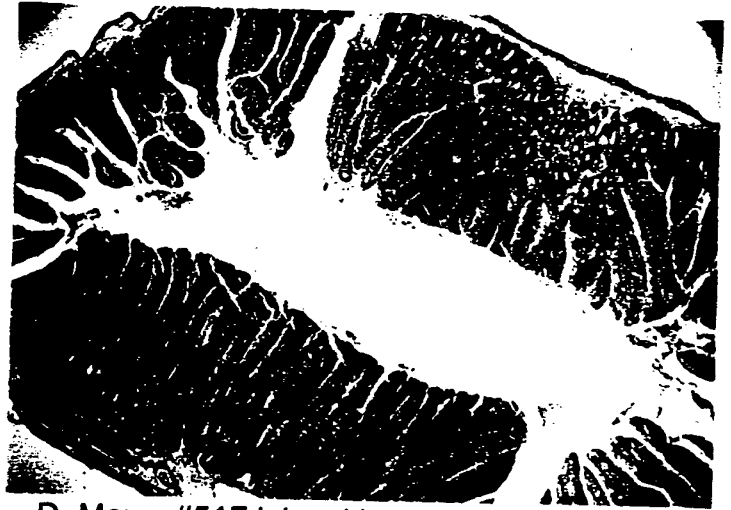
A. Control mouse#53F:duodenum, 40X



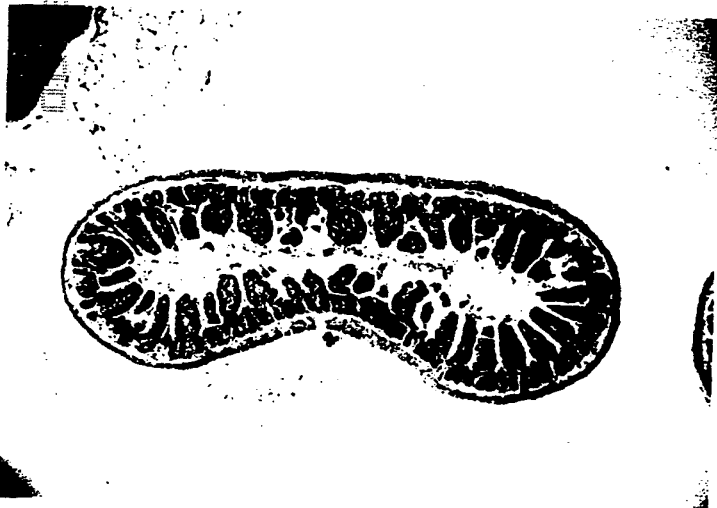
B. Mouse#51F:duodenum, 40X



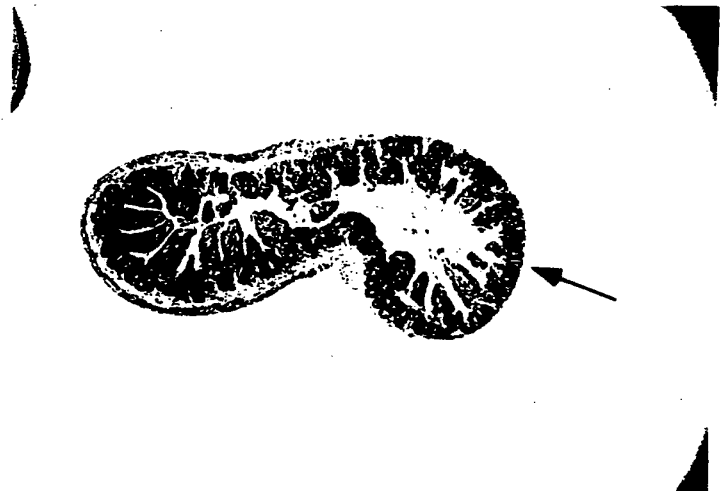
C. Control mouse#53F:jejunum, 40X



D. Mouse#51F:jejunal hyperplasia, 40X



E. Control mouse#53F:ileum, 40X



F. Mouse#231M:ileal atrophy, 40X

Figure 19



Figure 20

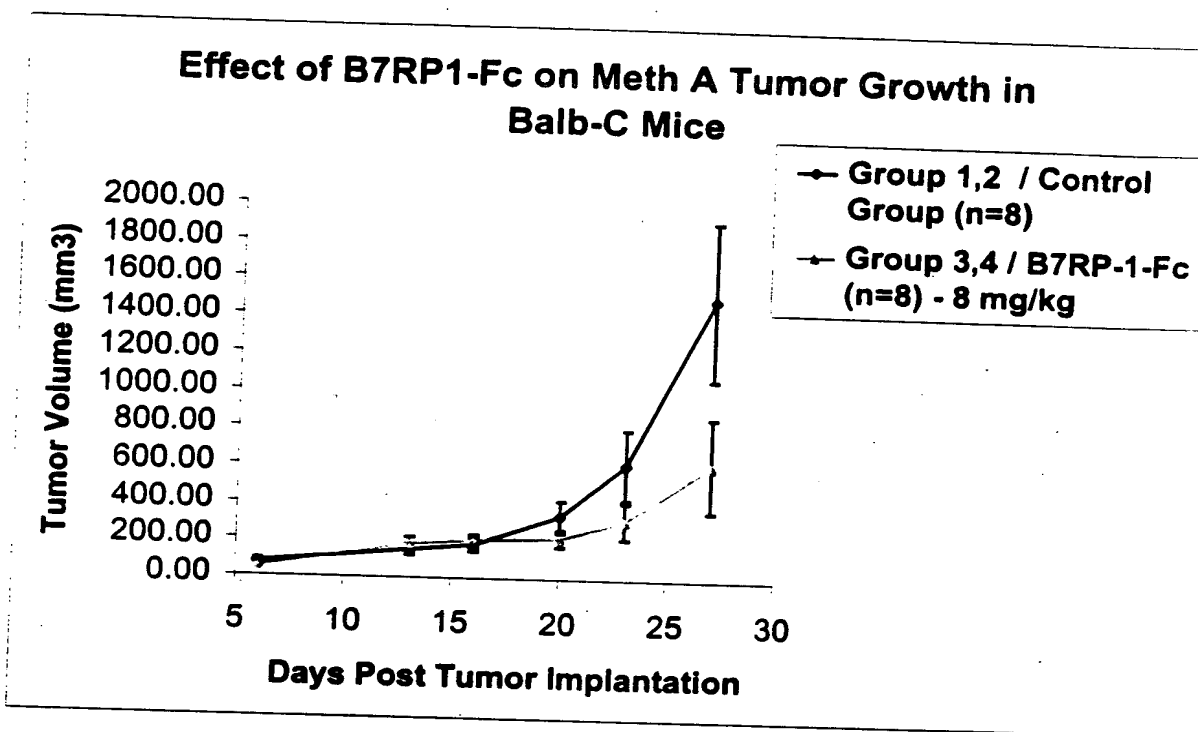




Figure 21A/B.

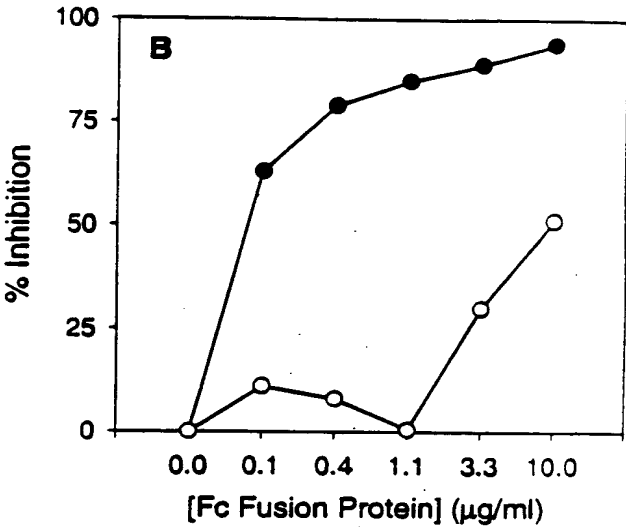
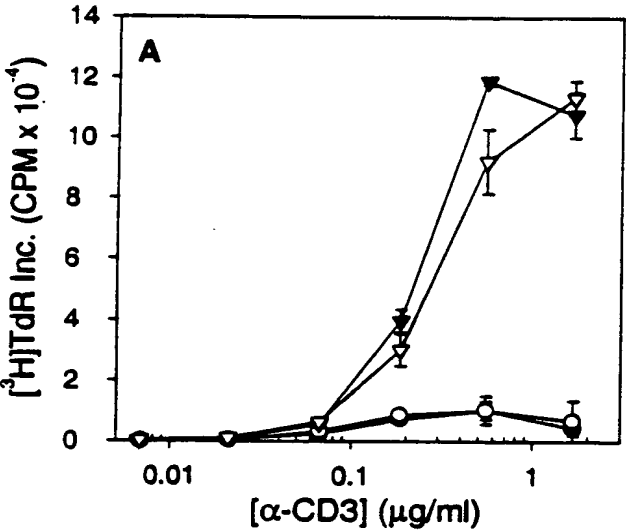




Figure 21C.

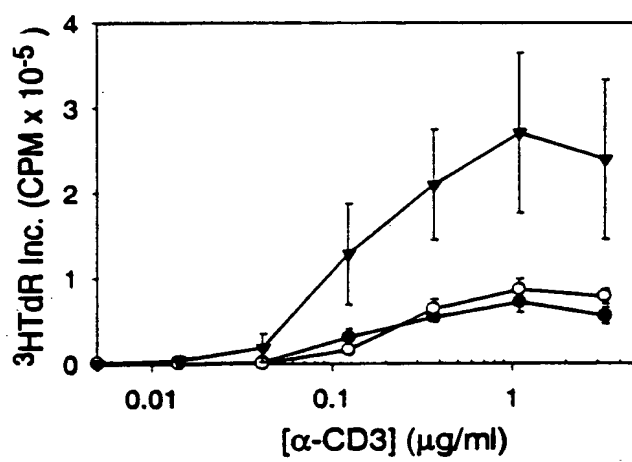




Figure 21D

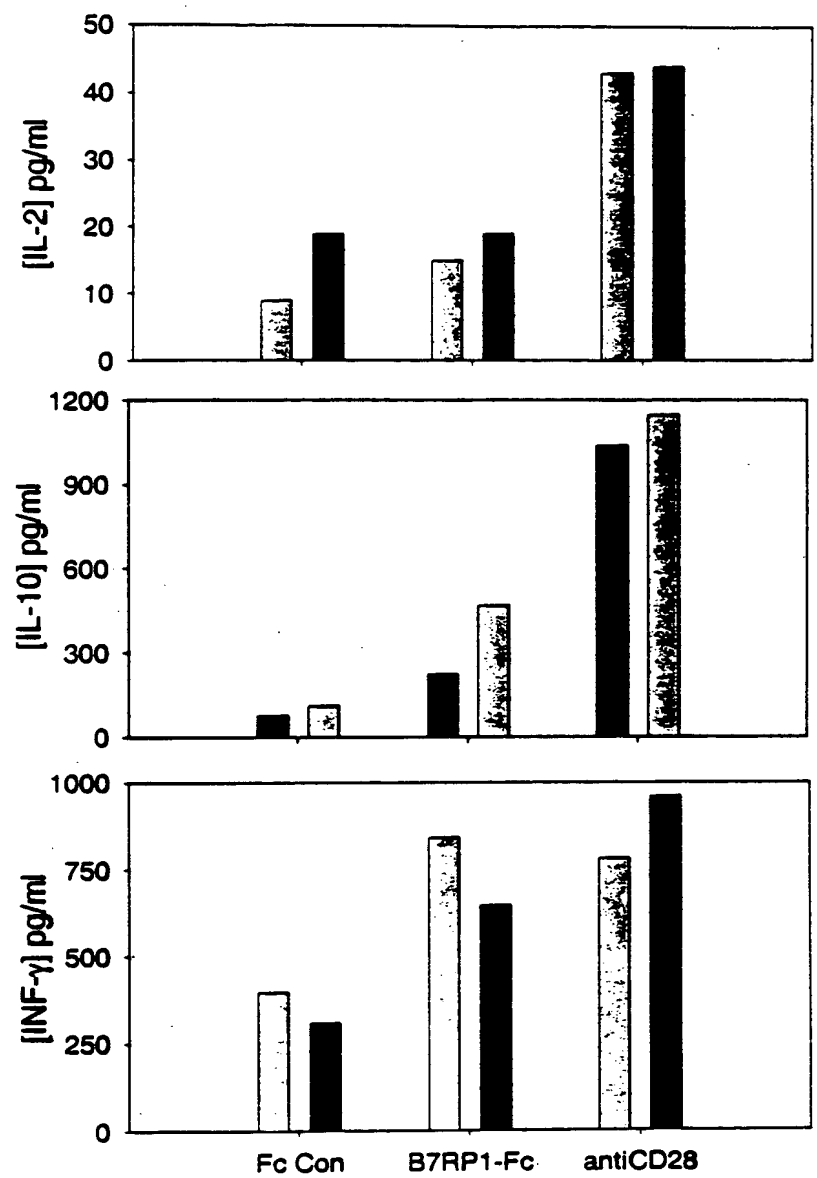








Figure 23

